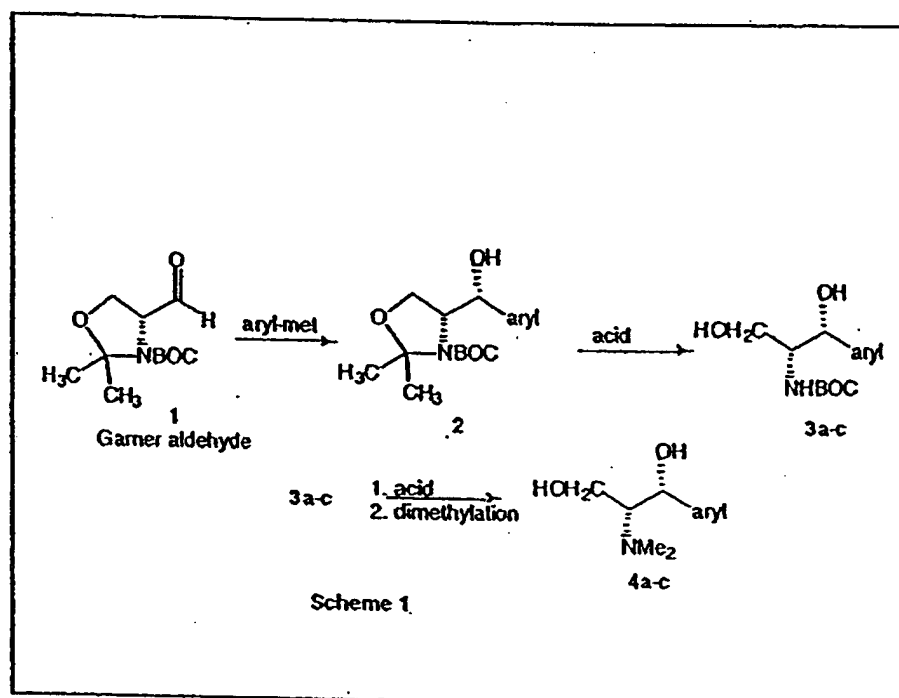


# Potential *Drosophila* SK Genes

181.	195	196	210	211	225	226	240	241	255	256	270
1 DSK1747	FRSSNDYGVNLOTAE	MAHTIRKHKR	----	-GNSSSPADCGKQL	LILLNPKSGSGKRE	LFKQVAPLLEAEV	QYOLQITTHPQYAKE	236			
2 DSK2159	FRSFOTFEDNIREAD	RMYSRLRMQLHRTLE	EIFVAPTVDERRRR	VLLNPKSGSGDARE	VFMHWTPVPLNEAEV	PYDLYVTKHSIFAIE	262				
3 HSPHK1	-----	-----	-----	-Y	VLLNPRGGKGAQ	LFRSHVQPLLAEEI	SFTLMLTERRNHARE	62			
271	285	286	300	301	315	316	330	331	345	346	360
1 DSK1747	FVTRRDLTRYSGI	WASGDGLFYEVING	LNERMDHRRACREL	P	LGIIPOGSGNGLAKS	VAHCHNEPYEKPIL	HATLTCHWAGK	--STP	324		
2 DSK2159	FLSTR--CLDAHCCV	VANGDGLFHEIVNG	LQRODHAHVLPHLA	LGIIPOGSGNGLARS	IAHCYNK-----	PVL	GAALTVISGR--SSP	343			
3 HSPHK1	LYRSE--ELGRWDAL	VMSGDGLMHEWING	LNERPDMETAIQKP	-	LCSLPAGSGNALAAS	LNIHVAGVEQVTNEDL	LTNCTLLCRRLISP	149			
361	375	376	390	391	405	406	420	421	435	436	450
1 DSK1747	MDVVRVELATROKHF	VMYSFLSVGNGLIAD	IDIESERLSRIGAOR	FTLWAIKRLIGLSY	KRVSYLLGKGKKEP	PVEAARELPAESTAA	414				
2 DSK2159	MDVVRVQLQSR	---	-LYSFLSIGNGLISD	VDIESERIMLVGYOR	FTWTLVRLVNLRTY	NGRISVILLTDHEVSS	-THSATGYAAQRVQ	428			
3 HSPHK1	MULLSLHTASGLR--	-LFSVLSLWNGFIAD	VOLESEKYRLGEMR	FTLGTFLRLAALRTY	RGRLAYLPVGRVSK	---TPASPIVVQ---	230				
451	465	466	480	481	495	496	510	511	525	526	540
1 DSK1747	GIRSSLPLNAGEFHD	LPEEEGEAVLDGEQ	FADAISLDRSY---	Y	RQWADSHHSANSRRT	AYSLGGPSHRSNRS	RKISQRTEAANAIEF	501			
2 DSK2159	SSRSCHTHIDMLNGP	APTYSSEAFLP-QE	FADVISLETISINQSF	RSRCDNLSGGRRS	FYYSIS-ESIYHSLA	DESEFAGLAASLEN	516				
3 HSPHK1	-QGPDVDAHLVPLEEP	VP-----	-----	-----	-----	-----	-----	246			
541	555	556	570	571	585	586	600	601	615	616	630
1 DSK1747	AER--VPTGTTPPLQ	NPLSSDGHICEDGD	FVMWHAAYTHLSSD	VFFAPESRLDDGLY	LVIIRRGVSRHQLLN	FMLNLNAGTHLPIGE	589				
2 DSK2159	RQNYGPASELPDLN	EPLSEDDQGLVEEGE	FVMWHAAYQTHLGD	CHFAPKAQLNDGTTY	LILIRAGISRHLLS	FLYNSSGTHLPESH	606				
3 HSPHK1	-----	-----	-SHMTVTPDED	FVLVLALLSHLHSGE	MFAAPVGRCAAGVWH	LFYIRAGVSRAMLLR	LFLANGKGRHMEY-E	315			
631	645	646	660	661	675	676	690	691	705	706	720
1 DSK1747	OPFIKVPICRAFRIE	PSSSDGILVDGERV	EYGPQAEVMPGLIN	VMTTSQ-----	-----	-----	-----	641			
2 DSK2159	DDHKVILPVRAFRL	PVDNIGIITVDGERV	EFGLPQAEVLPGIAR	VWVPNVSTFRFSAT	LQHGIPICIPVRKRF	VLNMSSEELAPINE	696				
3 HSPHK1	CPYLVTVPVWAFRL	PKDGKGFANDGELM	VSEAVGGQIHPIYFW	MUSGCVPEP--PSAK	PQMPPEEPL-----	-----	-----	384			

Fig. 1

Figure 2



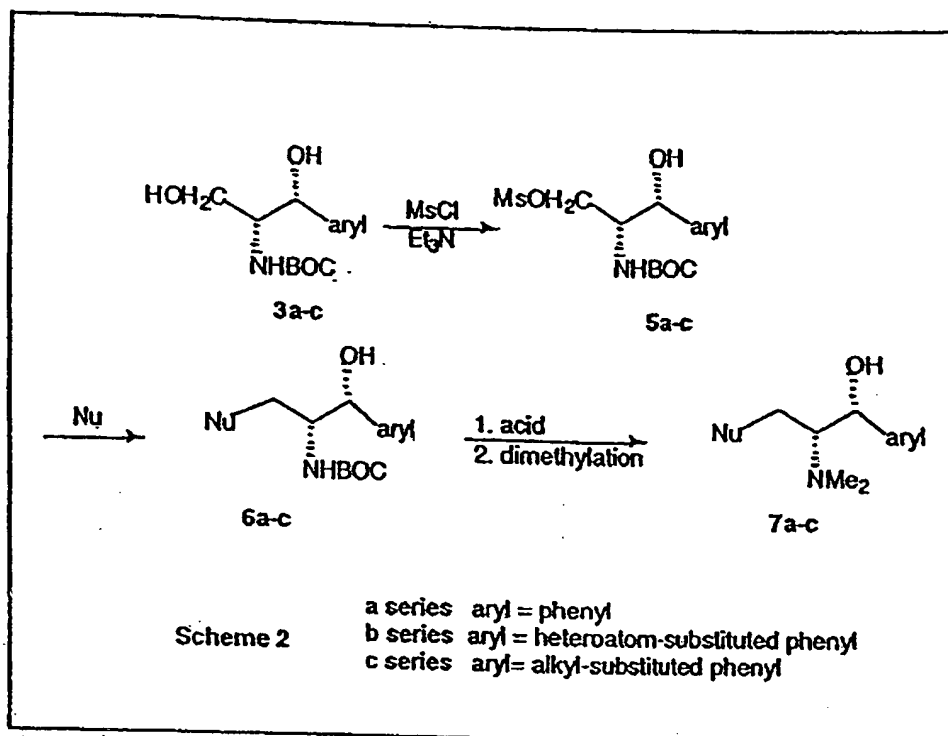


Figure 3

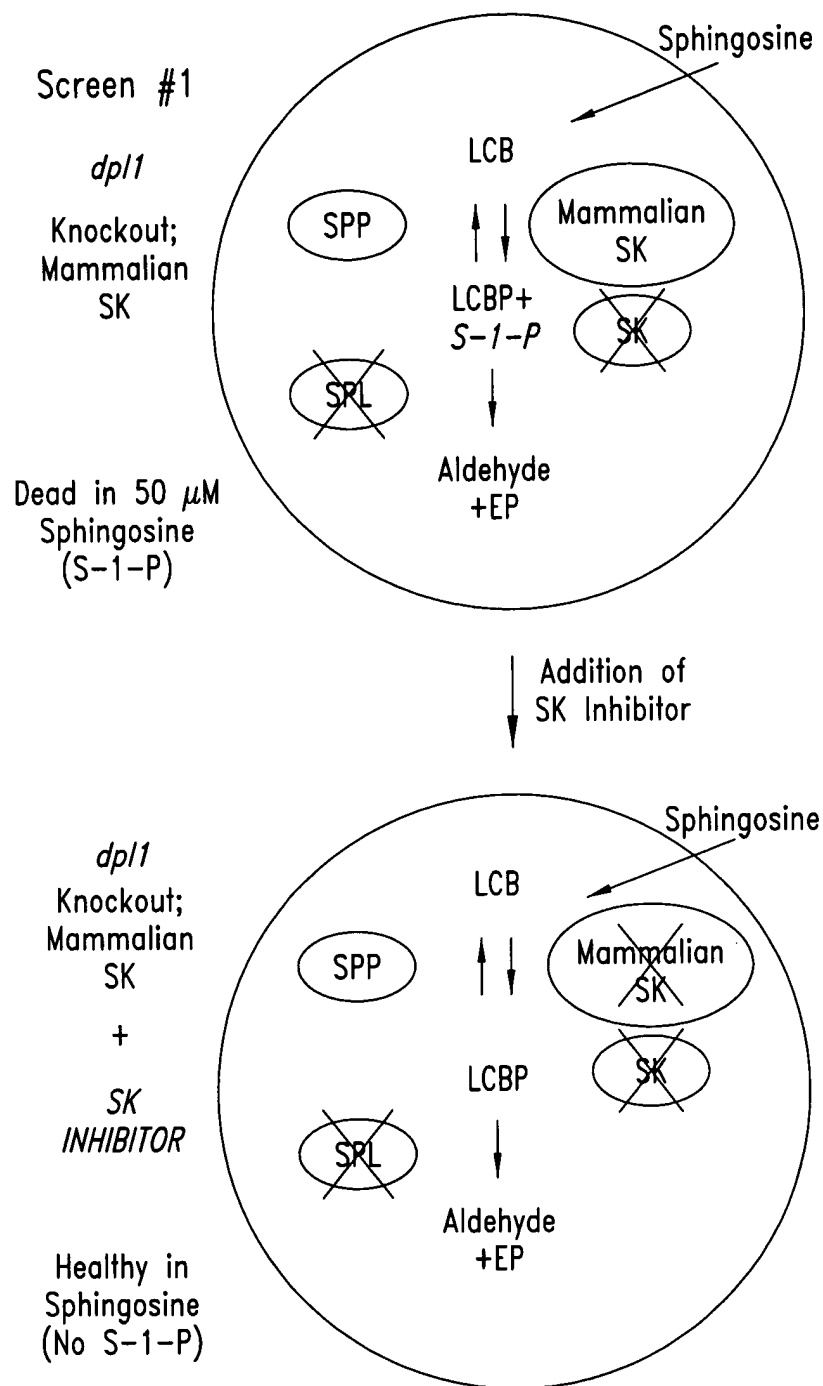


FIG. 4

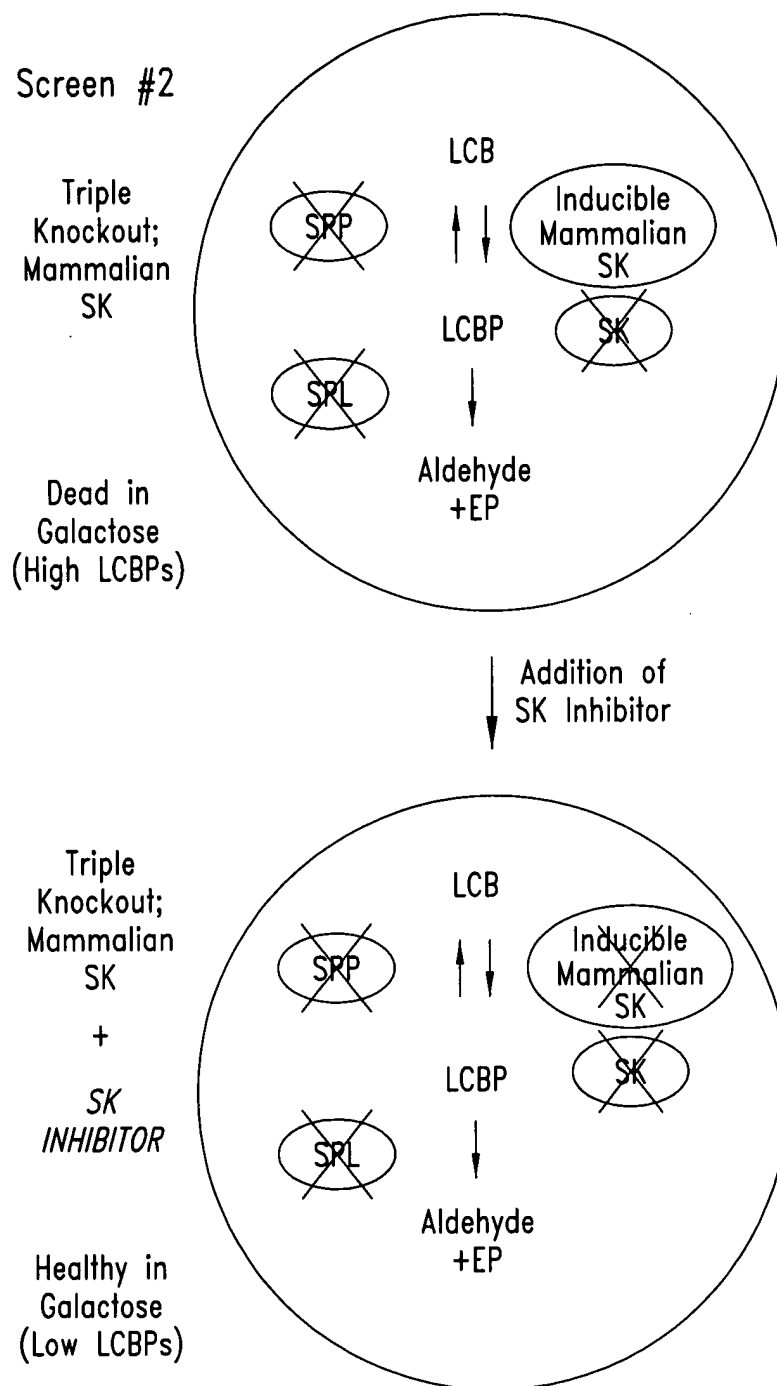


FIG. 5